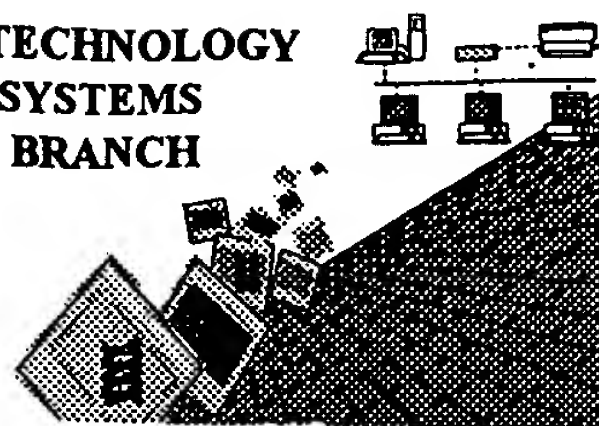


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

1652

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/697,186  
Source: 1600  
Date Processed by STIC: 2/22/2002

RECEIVED  
MAR 1 2 2002  
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/697,186

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
    Wrapped Aminos  
    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length  
    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino  
    Numbering  
    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII  
    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length  
    Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
    "bug"  
    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
    (OLD RULES)  
    Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
    (NEW RULES)  
    Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9 ☐ Use of n's or Xaa's  
    (NEW RULES)  
    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>  
    Response  
    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>  
    Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
    "bug"  
    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n  
    n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/697,186

DATE: 02/22/2002  
TIME: 14:56:40

Input Set: I697186.RAW

This Raw Listing contains the General  
Information Section and those Sequences  
containing ERRORS.

Does Not Comply  
Corrected Diskette Needed

1 <110> RIKEN  
2 <120> A MUTANT KANAMYCIN NUCLEOTIDYLTRANSFERASE AND A METHOD OF SCREENING  
3 THERMOPHILIC BACTERIA USING THE SAME  
4 <130> PH-1082  
5 <140> US/09/697,186  
6 <141> 2000-10-27  
7 <150> JP 11-309616  
8 <151> 29-OCT-1999  
9 <160> 11  
10 <170> PatentIn Ver. 2.0

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MAR 1 2 2002  
TECH CENTER 1600/2900

ppr 1-5

ERRORED SEQUENCES FOLLOW

E--&gt;

11 <210> 1  
12 <211> 253  
13 <212> PRT  
14 <213> Artificial Sequence  
15 <220>  
16 <223> mutantenzyme obtained by introduction of point mutation into wild type KNT  
17 gene of Staphylococcus aureus and its expression  
18 <400> 1  
19 Met Asn Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile Val  
20 1 5 10 15  
21 His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val Lys  
22 20 25 30  
23 Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro Tyr  
24 35 40 45  
25 Ser Asp Ile Glu Met Met Cys Val Met Ser Thr Glu Glu Ala Glu Phe  
26 50 55 60  
27 Ser His Glu Trp Thr Thr Gly Glu Trp Lys Val Glu Val Asn Phe Tyr  
28 65 70 75 80  
29 Ser Glu Glu Ile Leu Leu Asp Tyr Ala Ser Gln Val Glu Ser Asp Trp  
30 85 90 95  
31 Pro Leu Thr His Gly Gln Phe Phe Ser Ile Leu Pro Ile Tyr Asp Ser  
32 100 105 110  
33 Gly Gly Tyr Leu Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu Ala  
34 115 120 125  
35 Gln Lys Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu Phe  
36 130 135 140  
37 Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr Thr  
38 145 150 155 160  
39 Phe Leu Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met Leu

misaligned  
amino  
acid  
numbers  
(see  
item 3  
on Error  
summary  
sheet)

PAGE: 2

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/697,186DATE: 02/22/2002  
TIME: 14:56:40

Input Set: I697186.RAW

40                                   165                                   170                                   175  
41           Ile Gly Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val Leu  
42                                   180                                   185                                   190  
43           Thr Glu Ala Val Lys Gln Ser Asp Leu Pro Ser Gly Tyr Asp His Leu  
44                                   195                                   200                                   205  
45           Cys Gln Phe Val Met Ser Gly Gln Leu Ser Asp Ser Glu Lys Leu Leu  
46                                   210                                   215                                   220  
47           Glu Ser Leu Glu Asn Phe Trp Asn Gly Ile Gln Glu Trp Thr Glu Arg  
48           225                                   230                                   235                                   240  
49           His Gly Tyr Ile Val Asp Val Ser Lys Arg Ile Pro Phe  
50                                   245                                   250

51 <210> 3  
52 <211> 253  
53 <212> PRT  
54 <213> Artificial@Sequence  
55 <220>  
56 <223> mutant@enzyme@obtained@by@introduction@of@point mutation into wild  
57           type KNT@gene of Staphylococcus aureus and its@expression  
58 <400> 3  
59           Met Lys Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile Val  
60                                   1                                   5                                   10                                   15  
61           His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val Lys  
62                                   20                                   25                                   30  
63           Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro Tyr  
64                                   35                                   40                                   45  
65           Ser Asp Ile Glu Met Met Cys Val Leu Ser Thr Glu Gly Val Glu Phe  
66                                   50                                   55 @@@@ @@@@60  
67           Ser Tyr Glu Trp Thr Thr Gly Glu Trp Lys Ala Glu Val Asn Phe Tyr  
68                                   65                                   70                                   75                                   80  
69           Ser Glu Glu Ile Leu Leu Asp Tyr Ala Ser Arg Val Glu Pro Asp Trp  
70                                   85                                   90                                   95  
71           Pro Leu Thr His Gly Arg Phe Phe Ser Ile Leu Pro Ile Tyr Asp Pro  
72                                   100                                   105                                   110  
73           Gly Gly Tyr Phe Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu Ala  
74                                   115                                   120                                   125  
75           Gln Lys Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu Phe  
76                                   130                                   135                                   140  
77           Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr Thr  
78                                   145                                   150                                   155                                   160  
79           Phe Leu Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met Leu  
80                                   165                                   170                                   175  
81           Ile Gly Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val Leu  
82                                   180                                   185                                   190  
83           Thr Glu Ala Val Lys Gln Pro Asp Leu Pro Pro Gly Tyr Val Gln Leu  
84                                   195                                   200                                   205  
85           Cys Gln Leu Val Met Ser Gly Gln Leu Ser Asp Pro Glu Lys Leu Leu  
86                                   210                                   215                                   220  
87           Glu Ser Leu Glu Asn Phe Trp Asn Gly Val Gln Glu Trp Ala Glu Arg  
88                                   225                                   230                                   235                                   240

E--&gt;

*delete these non-ASCII characters globally**they cause errors.**misaligned nos.*

PAGE: 3

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/697,186

DATE: 02/22/2002  
TIME: 14:56:40

Input Set: I697186.RAW

89 His Gly Tyr Ile Val Asp Val Ser Lys Arg Ile Pro Phe  
90 245 250

91 <210> 10  
 E--> 92 <211> 759  
 93 <212> DNA  
 94 <213> Staphylococcus aureus  
 95 <220>  
 96 <221> CDS  
 97 <222> (1)..(759)  
 98 <400> 10  
 E--> 99 gtg aat gga cca ata ata atg act aga gaa gaa aga atg aag att gtt 48 Met  
 W--> 100  
 101 Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile  
 W--> 102 1 5 10 15  
 E--> 103 cat gaa att aag gaa cga ata ttg gat aaa tat ggg gat gat gtt aag 96 His  
 W--> 104  
 105 Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val  
 W--> 106 20 25 30  
 E--> 107 gct att ggt gtt tat ggc tct ctt ggt cgt cag act gat ggg ccc tat 144 Ala  
 W--> 108  
 109 Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro  
 110 35 40 45  
 E--> 111 tcg gat att gag atg atg tgt gtc atg tca aca gag gaa gca gag ttc 192 Ser  
 W--> 112  
 113 Ile Glu Met Met Cys Val Met Ser Thr Glu Glu Ala Glu  
 114 50 55 60  
 E--> 115 agc cat gaa tgg aca acc ggt gag tgg aag gtg gaa gtg aat ttt gat 240 Ser  
 W--> 116  
 117 Glu Trp Thr Thr Gly Glu Trp Lys Val Glu Val Asn Phe  
 W--> 118 65 70 75 80  
 E--> 119 agc gaa gag att cta cta gat tat gca tct cag gtg gaa tca gat tgg 288 Ser  
 W--> 120  
 121 Glu Ile Leu Leu Asp Tyr Ala Ser Gln Val Glu Ser Asp  
 W--> 122 85 90 95  
 E--> 123 ccg ctt aca cat ggt caa ttt ttc tct att ttg ccg att tat gat tca 336 Pro  
 W--> 124  
 125 Thr His Gly Gln Phe Phe Ser Ile Leu Pro Ile Tyr Asp  
 126 100 105 110  
 E--> 127 ggt gga tac tta gag aaa gtg tat caa act gct aaa tcg gta gaa gcc 384 Gly  
 W--> 128  
 129 Tyr Leu Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu  
 130 115 120 125  
 E--> 131 caa acg ttc cac gat gcg att tgt gcc ctt atc gta gaa gag ctg ttt 432 Gln  
 W--> 132  
 133 Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu  
 134 130 135 140  
 E--> 135 gaa tat gca ggc aaa tgg cgt aat att cgt gtg caa gga ccg aca aca 480 Glu  
 W--> 136  
 137 Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr

*delete*

*see p. 4*

*Insert hard return*

PAGE: 4

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/697,186

DATE: 02/22/2002  
TIME: 14:56:40

Input Set: I697186.RAW

W-->	138	145	150	155	160	
E-->	139	ttt cta cca tcc ttg act gta cag gta gca atg gca ggt gcc atg ttg	528 Phe			
W-->	140					
	141	Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met				
W-->	142	165	170	175		
E-->	143	att ggt ctg cat cat cgc atc tgt tat acg acg agc gct tcg gtc tta	576 Ile			
W-->	144					
	145	Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val				
	146	180	185	190		
E-->	147	act gaa gca gtt aag caa tca gat ctt cct tca ggt tat gac cat ctg	624 Thr			
W-->	148					
	149	Ala Val Lys Gln Ser Asp Leu Pro Ser Gly Tyr Asp His				
	150	195	200	205		
E-->	151	tgc cag ttc gta atg tct ggt caa ctt tcc gac tct gag aaa ctt ctg	672 Cys			
W-->	152					
	153	Phe Val Met Ser Gly Gln Leu Ser Asp Ser Glu Lys Leu				
	154	210	215	220		
E-->	155	gaa tcg cta gag aat ttc tgg aat ggg att cag gag tgg aca gaa cga	720 Glu			
W-->	156					
	157	Leu Glu Asn Phe Trp Asn Gly Ile Gln Glu Trp Thr Glu				
W-->	158	225	230	235	240	
E-->	159	cac gga tat ata gtg gat gtg tca aaa cgc ata cca ttt	759 His			
W-->	160					
	161	Tyr Ile Val Asp Val Ser Lys Arg Ile Pro				
W-->	162	245	250			

E--> 163 <210> 11 ? Please ensure 253 amino acids are shown in this sequence.  
 164 <211> 253 delete  
 165 <212> PRT see P5  
 166 <213> Staphylococcus aureus  
 167 <400> 11  
 168 Met Asn Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile  
 169 1 5 10 15  
 170 His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val  
 171 20 25 30  
 172 Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro  
 173 35 40 45  
 174 Ser Asp Ile Glu Met Met Cys Val Met Ser Thr Glu Glu Ala Glu  
 175 50 55 60  
 176 Ser His Glu Trp Thr Thr Gly Glu Trp Lys Val Glu Val Asn Phe  
 177 65 70 75  
 178 Ser Glu Glu Ile Leu Leu Asp Tyr Ala Ser Gln Val Glu Ser Asp  
 179 85 90 95  
 180 Pro Leu Thr His Gly Gln Phe Phe Ser Ile Leu Pro Ile Tyr Asp  
 181 100 105 110  
 182 Gly Gly Tyr Leu Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu  
 183 115 120 125  
 184 Gln Thr Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu  
 185 130 135 140  
 186 Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr

80 misaligned  
NOS.



PAGE: 5

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/697,186DATE: 02/22/2002  
TIME: 14:56:40

Input Set: I697186.RAW

187	145	150	155	160											
188	Phe	Leu	Pro	Ser	Leu	Thr	Val	Gln	Val	Ala	Met	Ala	Gly	Ala	Met
189				165						170					175
190	Ile	Gly	Leu	His	His	Arg	Ile	Cys	Tyr	Thr	Thr	Ser	Ala	Ser	Val
191				180						185					190
192	Thr	Glu	Ala	Val	Lys	Gln	Ser	Asp	Leu	Pro	Ser	Gly	Tyr	Asp	His
193				195						200				205	
194	Cys	Gln	Phe	Val	Met	Ser	Gly	Gln	Leu	Ser	Asp	Ser	Glu	Lys	Leu
195				210						215				220	
196	Glu	Ser	Leu	Glu	Asn	Phe	Trp	Asn	Gly	Ile	Gln	Glu	Trp	Thr	Gly
197				225						230				235	240
198	His	Gly	Tyr	Ile	Val	Asp	Val	Ser	Lys	Arg	Ile	Pro			
199					245					250					

E--> 200  
E--> 201

@@@

1/14

delete

misaligned  
nos.

Input Set: I697186.RAW

[illegible]



107 E Wrong Amino Acid Designator  
107 E Wrong Amino Acid Designator  
107 E Wrong Amino Acid Designator

gct att ggt gtt tat ggc tct ctt ggt cgt c  
gct att ggt gtt tat ggc tct ctt ggt cgt c  
gct att ggt gtt tat ggc tct ctt ggt cgt c

Input Set: I697186.RAW

[illegible]

Input Set: **I697186.RAW**

[illegible]

Input Set: I697186.RAW

[illegible]

143 E Wrong Amino Acid Designator

att ggt ctg cat cat cgc atc tgt tat acg a



Input Set: I697186.RAW

[illegible]



Input Set: I697186.RAW

Line	? Error/Warning	Original Text
156	W Invalid/Missing Amino Acid Numbering	
158	W Invalid/Missing Amino Acid Numbering	225 230 2
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
160	W Invalid/Missing Amino Acid Numbering	
162	W Invalid/Missing Amino Acid Numbering	245 250
164	E Input 253, Calc Seq.Length 254 differ	<211> 253
200	E Wrong Amino Acid Designator	@@@
201	E Invalid/Missing Amino Acid Numbering	1/14